

REMARKS

Initially, Applicant thanks the Examiner for conducting a telephonic interview on September 4, 2003. During the interview, the patentability of claims 1 and 3-10 was discussed, and possible amendments to independent claim 1 to overcome the prior art rejection of record. Specifically, it was agreed that the current amendment adding the limitation “of the two or more segment sequences” to claim 1 addressed the rejection, but that the Examiner would need to undertake additional searching in light of the amendment before allowing the claims.

Reconsideration and withdrawal of the rejections of record are respectfully requested.

Summary of Status of Amendments and Office Action

In the present amendment, claims 1, 5 and 7 are amended. Claims 2 and 11-20 have been previously canceled. Therefore, claims 1 and 3-10 are pending in the application with claim 1 being independent.

Claims 3 and 5-7 are objected to under 37 CFR 1.75(c) as being of improper dependent form.

Claims 1 and 3-10 are rejected under 35 U.S.C. § 112, second paragraph as being indefinite.

Claims 1 and 3-10 are rejected under 35 U.S.C. § 102(b) as being anticipated by Eisenberg et al. (U.S. Patent No. 5,436,580).

Response to Claim Objection Under 37 CFR 1.75(c)

Claims 3 and 5-7 are objected to under 37 CFR 1.75(c) as being of improper dependent form.

The Office Action asserts that claims 3 and 5-7 are dependent on claim 1, but improperly broaden

the scope of the claims by becoming drawn to a method of employing segmentation of a reference protein into one or more segment sequences.

In response, Applicant initially notes that, contrary to the Office Action's assertion, claim 3 does not broaden claim 1. Instead, the plain language of claim 3 states that the amino acid sequence of each "reference protein[] is divided into one or more core segment sequences which are predetermined to form a hydrophobic core, **and** into one or more sub segment sequences which are not predetermined to form a hydrophobic core." Claim 3 does not merely segment "a reference protein into one or more segment sequences" but instead segments the reference protein into "one or more core segment sequences which are predetermined to form a hydrophobic core, **and** into one or more sub segment sequences." Therefore, Applicant respectfully requests that the objection to claim 3 be reconsidered and withdrawn.

With respect to the objection to claims 5 and 7, the current amendment changes the language "one or more" to "two or more," thereby mooting the objection, and Applicant respectfully requests that the objection to these claims be withdrawn.

Response to § 112, Second Paragraph Rejections

Claims 1 and 3-10 are rejected under 35 U.S.C. § 112, second paragraph as being indefinite. The Office Action asserts that claims 1 and 3-10 are indefinite for use of the term "continuous amino acid residues." The Office Action interpreted the term as "contiguous." In response, Applicant notes that the term has been changed to contiguous.

The Office Action asserts that claims 1 and 3-10 are indefinite for use of the term “reference proteins that has high similarity in three-dimensional structure to the protein comprising the query sequence” because it is unclear what criteria is used to determine the similarity step. Additionally, it is asserted that it is unclear what degree of sequence homology between the query protein and the reference protein would be considered high.

In response, Applicant directs the Examiner’s attention to pages 15-25 of the specification, which describes Applicant’s invention, and specifically to pages 20-23 which discusses calculation of the matching score. Page 20 discusses the criteria for selecting the equation to be used for the calculation of a matching score and page 21 sets forth the criteria for one example of the calculation of the matching score. The specification makes clear that this example is but one possible way to calculate the similarity between the reference protein and the query protein. Applicant also notes that the specification at page 23 discusses the selection of a template candidate protein by comparing scores. Applicant respectfully submits that the teachings of the specification show that candidate proteins with a “high” similarity score will be those which have the highest scores. Applicant respectfully submits that the specification sets forth sufficient information to particularly point out and distinctly claim the subject matter applicant regards as the invention, and this basis for the rejection of claims 1 and 3-10 should be withdrawn.

The Office Action also asserts that claim 7 is indefinite for the use of the phrase “matching by sliding one or more core segment sequences on the query sequence” because it is unclear what is being slid against the query sequence. In response, Applicant respectfully directs the Examiner’s attention to pages 18-19 of the specification which discuss the matching of the candidate protein to

the query protein to determine the best matching score. Applicant submits that the teaching of the specification is clear, a segment sequence is slid down the query protein sequence until the best matching score is found. From this teaching, it is clear that the term “sliding” means simply that the segment sequence of the candidate protein is moved, or slid, down the query sequence until the segment sequence having the highest similarity is discovered. Applicant respectfully submits that the term is not indefinite and this rejection should be withdrawn.

The Office Action also asserts that claim 8 is indefinite for the use of the phrase “the optimum matching” because there is insufficient antecedent basis for this limitation. Further, the Office Action asserts that the term “calculated scores obtained from environmental information” is indefinite because it is unclear what criteria the scores were derived. In response, Applicant amended the claim to more clearly set forth the subject matter of the claim. Specifically, Applicant amended the term “the optimum matching” to “an optimum matching” to show that the optimum matching is the end product of the method of the claimed invention of claim 8. With respect to the second basis for the rejection, Applicant directs the Examiner’s attention to pages 19-22 of the specification which discusses the criteria for determining the matching score, and from these scores, determining the optimum matching. Applicant respectfully submits that in light of the teachings of the specification, claim 8 is not indefinite and this rejection should be withdrawn.

Finally, the Office Action asserts that claim 10 is indefinite because it is unclear when the three-dimensional structure of the protein can be established. In response, Applicant respectfully directs the Examiner’s attention to pages 14-25 of the specification setting forth an example of the claimed method. More specifically, page 23-25 of the specification discusses the construction of a

three-dimensional structure of the query protein as the final step in the claimed method after the optimum matching scores for the segment sequences have been calculated. Therefore, Applicant respectfully submits that in light of the teachings of the specification, claim 10 is not indefinite and this rejection should be withdrawn.

For these reasons, Applicant respectfully requests that the Examiner withdraw the rejections of claims 1 and 3-10 under 35 U.S.C. § 112, second paragraph.

Response to § 102(b) Rejection

Claims 1 and 3-11 are rejected under 35 U.S.C. § 102(a) as being anticipated by Eisenberg et al. (U.S. Patent No. 5,436,850). The previous Office Actions asserted that Eisenberg ('850) teaches a method of identifying a protein's sequence that folds into a predetermined 3-D structure and that the claims require two or more segments of the reference protein for establishing the environmental information, but the segments themselves are not explicitly required for their comparison against the query protein. In response, Applicant amended claim 1 to recite that the matching is based on the environmental information on each amino acid residue of each of the two or more segment sequences of the reference protein and hydrophobicity or hydrophilicity property of the side chain of each amino acid residue of the query sequence.

The current Office Action asserts that Eisenberg ('850) discloses a method of determining the backbone structure of a query protein by comparing its sequence against a database of reference proteins and compares the environmental string of the proteins and assigns various classes for each residue. The Office Action asserts that Eisenberg ('850) discloses that all sequences are aligned with

the 3D structure profile using a dynamic programming, which allows insertions and deletion. The Office Action notes that Eisenberg ('850) does not explicitly disclose that the comparison of the sequences involves the segmentation of the reference protein into two or more segments, wherein the segments comprise two or more contiguous amino acid sequences. However, the Office Action asserts that Eisenberg (U.S. Patent No. 6,512,981) discloses the allegedly inherent property of dynamic programming algorithm which the '850 patent employs. The Office Action asserts that Eisenberg ('850) inherently anticipates the claimed invention because it employs a dynamic programming as shown in Eisenberg ('981).

Initially, Applicant notes that the rejection does not point to any teaching in Eisenberg ('850) which discusses its use of "a dynamic programming algorithm" in the disclosed method. Instead, the Office Action points to the teachings in an **unrelated** patent, whose provisional application was filed more than two years after the issuance of Eisenberg ('850), as supporting the assertion that Eisenberg ('850) used this method. This assertion is utterly without basis. Moreover, the Eisenberg ('981) inventors must have felt that this "dynamic programming algorithm" allegedly inherent in Eisenberg ('850) was not disclosed, as this is the substance of the claims of the '981 patent. The Office Action's rejections of claims 1 and 3-10 as inherently anticipated by Eisenberg ('850) is meritless, and should be withdrawn.

Furthermore, to prove anticipation by inherency, the Examiner must show evidence which "must make clear that the missing descriptive matter is necessarily present in the thing described in the reference, and that it would be so recognized by persons of ordinary skill." Continental Can Co. USA v. Monsanto Co., 948 F.2d 1264, 1268 (Fed. Cir. 1991). Applicant respectfully submits that

the rejection fails to make this required showing. The Office Action does not point to any teaching in Eisenberg ('850) which shows that the method claimed in Eisenberg ('981), a "dynamic programming algorithm," was necessarily present in Eisenberg ('850). This is because it was not present in Eisenberg ('850), as shown by the Eisenberg ('981) inventors need to patent this "dynamic programming algorithm." Finally, the Office Action does not state that one of ordinary skill in the art would have recognized that the method claimed in Eisenberg ('981) was necessarily present in Eisenberg ('850), nor could it make such an assertion in light of the facts. The Office Action has failed to meet its burden for making the inherency rejection, and the rejection should be withdrawn.

Therefore, in view of the above, Applicant respectfully requests that the Examiner reconsider and withdraw the rejection of claims 1 and 3-10 under 35 U.S.C. § 102(b).

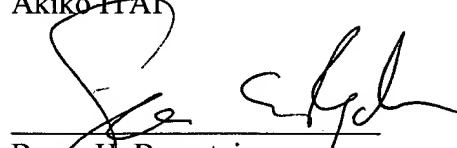
CONCLUSION

In view of the forgoing, Applicant respectfully submits that all pending claims patentably define Applicant's invention. Allowance of the application with an early mailing date of the Notices of Allowance and Allowability is therefore respectfully requested.

Any comments or questions concerning this application can be directed to the undersigned at the telephone number given below.

Respectfully submitted,

Akiko ITAI


Bruce H. Bernstein
Reg. No. 29,027


Reg. No.
45905

June 21, 2004
GREENBLUM & BERNSTEIN, P.L.C.
1950 Roland Clarke Place
Reston, VA 20191
(703) 716-1191